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					22041-22247 25096-25193 25336-25751 26609-26714 26798-27211 28295-28832 29914-30366 31336-31510 31520-32202 33873-33965 34131-34431 34675-34784 35103-35705 36242-36731 36873-37401 37440-37680 37699-41271 41712-50442
HBJDZ49	9502	847928	AF030453	42364	1-64 232-342 1337-1852 2559-2964 3673-7264 7293-7508 7746-7780 7953-18188
HBJDZ49	9502	847928	AC004867	42365	1-1716 2250-2502 2834-3813 5396-5483 5650-5950 6624-7332 7837-8257 8379-11753 11756-12384 12781-13088 13239-13304 13326-17824 17886-18086 18320-21988 22072-23613
HBJDZ49	9502	847928	AC005088	42366	1-91 259-371 1378-1894 2601-3006 3715-7552 7788-7822 7995-12991 13010-18252
HBJDZ49	9502	847928	AC005488	42367	1-1525 2823-3802 5381-5467 5634-5934 7010-7619 7948-8368 8868-11864 11870-12107

					12594-12811 12884-13191 13225-13414 13437-14521 14529-17110 17190-17916 17924-21107 21551-23569 23842-24790 25294-25593 25666-26072 27692-27800 27845-28102 28538-29666 30322-30463 30913-31471 33356-33443 33610-33910 34799-35052 35063-35484 36553-37367 38056-39110
HBJDZ49	9502	847928	AC005098	42368	1-1716 2360-2501 2897-3814 5395-5482 5649-5949 6624-7332 7837-8257 8530-11755 11758-12386 12495-12713 12792-13099 13250-13315 13337-17835 17902-18103 18336-22003 22097-24218
HBJDZ49	9502	847928	AC004166	42369	1-1716 2357-2498 2831-3810 5393-5480 5647-5947 6621-7329 7834-8254 8376-11750 11753-12381 12778-13085 13236-13301 13323-16669 16700-17821 17883-18016 18317-21985 22062-23603
HBJDZ49	9502	847928	AC005071	42370	1-1715 2229-2480 2882-3799

					5384-5472 5637-5962 6637-7520 7764-8274 8396-12010 13347-14042 14076-14293 14296-17861 17931-18121 18344-21358
HBJDZ49	9502	847928	AC061712	42371	1-103 1368-1977 2306-2726 2999-6224 6227-6464 6951-7168 7241-7548 7582-7771 7794-10119
HBJDZ49	9502	847928	AC007000	42372	1-2261 2328-3085 3093-6210 6306-6555 6630-8724 9378-10405 10433-10732 10766-11172 11591-11805 12605-13216
HBJDZ49	9502	847928	AC006995	42373	1-719
HBJDZ49	9502	847928	AC073967	42374	1-528
HBJDZ49	9502	847928	AC006014	42375	1-979
HBJDZ49	9502	847928	AC007003	42376	1-614
HBJDZ49	9502	847928	AC007000	42377	1-35 200-361 374-4630 4674-5056 5071-7020
HBJDZ49	9502	847928	AC073517	42378	1-583
HBJDZ49	9502	847928	AC006995	42379	1-1659
HBJDZ49	9502	847928	AC006014	42380	1-929 1161-4487 4579-5506 5664-5765 5979-9483 10048-10856 11336-11702 12041-12251 12253-12463 13816-13903 13917-14426
HBJDZ49	9502	847928	AC004878	42381	1-255
HBJDZ49	9502	847928	AC004878	42382	1-741 818-1073 1163-3038
HBJDZ49	9502	847928	AC004980	42383	1-293
HBJDZ49	9502	847928	AC004980	42384	1-1417

HBJDZ49	9502	847928	AC005073	42385	1-513 2138-2341 2878-3828 4039-4407 4438-5711 6598-6908 6969-7501 7547-7645 7882-8496 8569-9146 9288-11595 11642-11927 12146-12299 12591-12757 13029-13369 13719-14460 14563-14623 14696-15271 15352-16582 16831-17249 17276-17914 17947-18016 18327-19493 19719-20635 21271-22015 22432-22985 23034-23359 24795-25234 26499-26923 27475-28264 28742-29110 29565-29655 29657-29867 30539-30779 31272-31718
HBJDZ49	9502	847928	AC005073	42386	1-257
HBJDZ49	9502	847928	AC018720	42387	1-1380
HBJDZ49	9502	847928	AC006480	42388	1-1207
HBJDZ49	9502	847928	AC006480	42389	1-327
HBJDZ49	9502	847928	AF030453	42390	1-583
HBJDZ49	9502	847928	AF030453	42391	1-3119 3130-4112
HBJDZ49	9502	847928	AC004867	42392	1-868 1145-2855 2954-4494 4586-5798 5910-9476 10040-10848 11092-11171 11330-11695 12154-12509 13065-13372 13935-14448
HBJDZ49	9502	847928	AC004867	42393	1-583 834-1954
HBJDZ49	9502	847928	AC005088	42394	1-583
HBJDZ49	9502	847928	AC005088	42395	1-3121

					3128-4110
HBJDZ49	9502	847928	AC005488	42396	1-867 1144-2852 2949-4487 4579-5789 5978-9485 10048-10911 11334-11700 12034-12509 13205-13321 13907-14417
HBJDZ49	9502	847928	AC005488	42397	1-735 738-975
HBJDZ49	9502	847928	AC005098	42398	1-866 1143-2850 2949-4489 4581-5793 5905-8184 8255-9460 10026-10834 11078-11157 11307-11672 12131-12486 13183-13299 13912-14426
HBJDZ49	9502	847928	AC005098	42399	1-937
HBJDZ49	9502	847928	AC004166	42400	1-868 1146-2858 2957-4497 4589-5801 5913-9479 10043-10851 11095-11174 11333-11698 12157-12512 13938-14451
HBJDZ49	9502	847928	AC004166	42401	1-583 834-1954
HBJDZ49	9502	847928	AC005071	42402	1-896
HBJDZ49	9502	847928	AC061712	42403	1-1123 1396-3493 3581-3836 3838-7040 7048-8923
HBJDZ49	9502	847928	AC005071	42404	1-513 2138-2341 2878-3828 4039-4407 4438-5711 6609-6900 6969-7501 7547-7645 7882-8496 8569-9146 9288-11595 11642-11927 12146-12299

					12591-12757 13029-13369 13719-14460 14563-14623 14709-15271 15352-16582 16831-17249 17276-17914 17947-18016 18327-19493 19719-20635 21586-21816 24795-25126 26501-26923 27475-28264 28742-29110 29565-29655 29657-29867 31272-31718
HBJDR24	9503	677407	AC009951	42405	1-642
HBJDR24	9503	677407	AC009951	42406	1-327
HBJDR24	9503	677407	AC009951	42407	1-486 993-1122
HBJDQ86	9504	784654	AL133548	42408	1-50 3009-3073 4198-4253 5692-5831 6776-6827 8851-8970 9968-10050 12598-12974 13262-13364 16417-16776 19112-20566
HBJDQ86	9504	784654	AL133548	42409	1-1017
HBJDM70	9505	757435	AC010894	42410	1-380
HBJDM70	9505	757435	AC010894	42411	1-502
HBJDL24	9506	678272	AC008675	42412	1-996
HBJDL24	9506	678272	AC008675	42413	1-300
HBJCQ65	9508	876430	AF192303	42414	1-1230 1271-3810
HBJCJ82	9509	779645	AL161456	42415	1-1118
HBJCJ82	9509	779645	AL158075	42416	1-1523
HBJCJ82	9509	779645	AL158075	42417	1-853 1340-2553
HBJCJ82	9509	779645	AL158075	42418	1-482
HBJCE07	9510	954090	AC025605	42419	1-357 443-919
HBJCE07	9510	954090	AC073101	42420	1-357
HBJCE07	9510	954090	AC025605	42421	1-653
HBJCE07	9510	954090	AC073101	42422	1-233
HBJCE07	9510	954090	AC073101	42423	1-420
HBJBR04	9512	847952	AC005682	42424	1-458
HBJBR04	9512	847952	AC005682	42425	1-373
HBJAP95	9513	796659	AL138715	42426	1-1044
HBJAP95	9513	796659	AL031601	42427	1-590 1338-1600

					2644-3247
HBJAP95	9513	796659	AL138715	42428	1-717
HBJAP95	9513	796659	AL138715	42429	1-265
HBJAP95	9513	796659	AL031601	42430	1-706
HBJAJ49	9515	723164	AC078846	42431	1-416 1103-1882
HBJAJ49	9515	723164	AC078846	42432	1-116
HBJAH27	9517	682941	AC016325	42433	1-69 560-632 2298-2395 2510-2613 3563-3801 5031-5598 5763-5801
HBJAE32	9518	699695	AC044843	42434	1-487 983-1447
HBJAE32	9518	699695	AC008525	42435	1-487 983-1447
HBJAE32	9518	699695	AC008525	42436	1-337
HBJAB49	9520	722195	AF276759	42437	1-1613
HBJAB49	9520	722195	AC019031	42438	1-1613
HBJAB49	9520	722195	AF276759	42439	1-561
HBJAB49	9520	722195	AC019031	42440	1-561
HBJAB28	9521	847966	AC023071	42441	1-736
HBJAB15	9522	660552	AP001931	42442	1-1266
HBJAB15	9522	660552	AP000727	42443	1-1264
HBJAB15	9522	660552	AP001931	42444	1-366
HBJAB15	9522	660552	AP001931	42445	1-308
HBJAB15	9522	660552	AP000727	42446	1-366
HBJAB15	9522	660552	AP000727	42447	1-308
HBDAE47	9523	720008	AL353776	42448	1-1591
HBDAE47	9523	720008	AL353776	42449	1-490
HBDAD16	9525	661560	AC013396	42450	1-1371
HBDAD16	9525	661560	AC013396	42451	1-296
HBDAD16	9525	661560	AC013396	42452	1-204
HBCCO10	9526	963157	AC009634	42453	1-575
HBCCO10	9526	963157	AC011721	42454	1-575
HBCCO10	9526	963157	AC009634	42455	1-206
HBCCO10	9526	963157	AC011721	42456	1-206
HBCCO10	9526	963157	AC011721	42457	1-86
HBCCJ05	9527	930956	AC068322	42458	1-600
HBCCJ05	9527	930956	AC027243	42459	1-600
HBCCJ05	9527	930956	AC024059	42460	1-600
HBCCJ05	9527	930956	AC010868	42461	1-584
HBCCJ05	9527	930956	AC068322	42462	1-424
HBCCJ05	9527	930956	AC027243	42463	1-456
HBCCJ05	9527	930956	AC068322	42464	1-460 1112-1585
HBCCJ05	9527	930956	AC027243	42465	1-460 1112-1585
HBCCJ05	9527	930956	AC024059	42466	1-456
HBCCJ05	9527	930956	AC010868	42467	1-385
HBCCJ05	9527	930956	AC010868	42468	1-335
HBCCD06	9529	938319	AC007783	42469	1-2334 2508-3084 3578-3890

					4198-4294 4376-4623 4712-5349 5369-6088 6527-7107 7298-7392 7730-7846 9147-9476 10487-10575 10791-11298 11485-11601 11783-13009 13207-13501 13540-13772 14439-14800 14923-14983 15133-15355 15485-15653 16750-16805 16894-17078 17162-17219 18003-18089 21085-21146 21358-21501
HBCCD06	9529	938319	AC007783	42470	1-308
HBCCD06	9529	938319	AC007783	42471	1-1024
HBCCB51	9530	975256	AL139353	42472	1-71 265-794 1791-2077 2409-2656
HBCBN51	9532	952057	AC073846	42473	1-141 323-951 1073-1625 1640-2371
HBCBN51	9532	952057	AC073846	42474	1-285
HBCBF12	9535	969578	AC068735	42475	1-530
HBCBF12	9535	969578	AC021725	42476	1-534
HBCBF12	9535	969578	AL021368	42477	1-382 762-1102 1231-1761
HBCBF12	9535	969578	AC068735	42478	1-342
HBCBF12	9535	969578	AC021725	42479	1-342
HBCBF12	9535	969578	AC068735	42480	1-659
HBCBF12	9535	969578	AC021725	42481	1-679
HBCBF12	9535	969578	AL021368	42482	1-664
HBCBF12	9535	969578	AL021368	42483	1-307
HBCBE57	9536	848322	AL031666	42484	1-1235
HBCBE57	9536	848322	AL031666	42485	1-508
HBCBE57	9536	848322	AL031666	42486	1-648
HBCBB22	9537	848325	AC010735	42487	1-900
HBCAT10	9539	968195	AL357521	42488	1-374
HBCAT10	9539	968195	AL021528	42489	1-374
HBCAT10	9539	968195	AL357521	42490	1-689
HBCAT10	9539	968195	AL357521	42491	1-355
HBCAT10	9539	968195	AL021528	42492	1-689
HBCAT10	9539	968195	AL021528	42493	1-355

HBCAS32	9540	699489	AC007101	42494	1-215 867-1214 1226-2260 2359-2415
HBCAQ85	9541	783431	AC019071	42495	1-831 1116-1365 1600-1920 2161-2334 2902-3156 3364-3836 4074-4278 4306-4417 4485-4581 4693-4853 4995-5264 5758-5863 6411-6509 6551-6922
HBCAQ85	9541	783431	AC019071	42496	1-412
HASCG58	9543	738423	AC011116	42497	1-869
HASCG58	9543	738423	AC078794	42498	1-870
HASCG58	9543	738423	AC011116	42499	1-971
HASCG58	9543	738423	AC078794	42500	1-623
HASCG58	9543	738423	AC011116	42501	1-623
HASAW90	9544	789112	AC010234	42502	1-2931
HASAW90	9544	789112	AC021464	42503	1-58 332-547 909-1209 2280-2634 3445-3539 4477-4620 7577-10496 12087-13447 13462-15091 15142-16137
HASAW90	9544	789112	AC021464	42504	1-506
HASAC10	9546	968746	AC007677	42505	1-477
HASAC10	9546	968746	AC007677	42506	1-1410

[052] Table 1B summarizes additional polynucleotides encompassed by the invention (including cDNA clones related to the sequences (Clone ID NO:Z), contig sequences (contig identifier (Contig ID:) contig nucleotide sequence identifiers (SEQ ID NO:X)), and genomic sequences (SEQ ID NO:B)). The first column provides a unique clone identifier, "Clone ID NO:Z", for a cDNA clone related to each contig sequence. The second column provides the sequence identifier, "SEQ ID NO:X", for each contig sequence. The third column provides a unique contig identifier, "Contig ID:" for each contig sequence. The fourth column, provides a BAC identifier "BAC ID NO:A" for the BAC clone referenced in the corresponding row of the table. The fifth column provides the nucleotide sequence identifier, "SEQ ID NO:B" for a fragment of the BAC clone identified in column four of the corresponding row of the table. The sixth column, "Exon From-To", provides the location (i.e., nucleotide position numbers) within the polynucleotide sequence of SEQ ID NO:B which delineate certain polynucleotides of the invention that are also exemplary members of polynucleotide sequences that encode polypeptides of the invention (e.g., polypeptides containing amino acid sequences encoded by the polynucleotide sequences delineated in column six, and fragments and variants thereof).

**TABLE 2**

Clone ID NO:Z	Contig ID:	SEQ ID: NO:X	Analysis Method	PFam/NR Description	PFam/NR Accession Number	Score/ Percent Identity	NT From	NT To
HAMHB21	961376	11	HMMER 2.1.1	PFAM: RhoGAP domain	PF00620	100	497	916
HBDAC79	935414	26	HMMER 2.1.1 blastx.14	PFAM: Acyl-CoA dehydrogenase (AL021958) fadE9 [Mycobacterium tuberculosis]	PF00441	102.6	94	342
HBIAG72	722723	32	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	gi 2911026 emb CAA 17519.1	62% 51% 64% 35%	94 250 348 6	255 384 422 89
HBJGT92	919507	107	HMMER 1.8	PFAM: Bacterial mutT protein	PF00099	2.32	83	115
HBJIY20	669519	141	HMMER 2.1.1	PFAM: Orn/Lys/Arg decarboxylase	PF01276	53.1	49	162
HBMBU24	677240	234	HMMER 1.8	PFAM: Core histones H2A, H2B, H3 and H4	PF00125	7.72	139	192
HBMBZ71	880580	238	HMMER 1.8	PFAM: von Willebrand factor type D domain	PF00094	26.52	200	526
HBMDC16	888206	258	blastx.2	Butyrophilin-like protein BUTR-1.	sp AAF72554 AAF72 554	50%	19	315
HBMUO90	928078	294	blastx.14	Zfp61p [Mus musculus]	gi 887887 gb AAC52 290.1	84% 53%	24 154	119 243
HBMXE31	573323	317	HMMER 1.8	PFAM: Gonadotropin-releasing hormones	PF00446	10.78	112	141
HCFCF47	894415	372	HMMER 1.8	PFAM: Eukaryotic protein kinase domain	PF00069	89.54	20	295
HCFCJ21	671028	374	HMMER	PFAM: Core histones	PF00125	12.79	123	188

HCFILE95	945122	391	1.8 blastx.14	H2A, H2B, H3 and H4 p34 protein [Rattus sp.]	gi 534876 dbj BAA02 786.1	81% 100% 85%	126 236 71	191 271 91
HCUAL07	953876	449	blastx.14	(AF079098) arginine-tRNA-protein transferase 1-1p; ATE1-1p [Homo sapiens]	gi 3806094 gb AAD1 2366.1	87%	5	97
HCUBJ11	967484	478	blastx.14	Ps 2=basic proline-rich protein(PRBI)L precursor 1 1 [Homo sapiens]	gi 386433 gb AAB27 289.1	37% 53% 35% 40%	158 62 325 133	63 24 242 59
						28% 40% 36% 36% 41% 41% 32% 33% 36% 36% 71% 71%	158 133 225 225 74 74 325 158 158 183 44 44	63 24 242 59 63 59 160 160 24 24 118 24 24
HCUDT65	915742	548	HMMER 2.1.1 blastx.14	PFAM: tRNA synthetases class II (A)	PF01411 gi 301892 emb CAA 95907.1	35.1 42% 52% 31% 42%	697 763 658 1153 1678	930 972 759 1293 1740

							21%	1009	1149
							20%	1273	1494
HCUEU10	964857	595	HMMER 1.8	PFAM: Bacterial regulatory proteins, luxR family	PF00196	5.43	13	42	
HCUGB48	880730	647	HMMER 1.8	PFAM: TNFR/NGFR cysteine-rich region	PF00020	7.99	173	226	
HCUGR38	706471	670	HMMER 1.8	PFAM: Alcohol/other dehydrogenases, short chain type	PF00106	73.02	102	284	
HCUJHM44	615198	702	HMMER 1.8	PFAM: HMG (high mobility group) box	PF00505	4.81	2	73	
HCWAK80	702435	748	HMMER 1.8	PFAM: Src homology domain 3	PF00018	3.55	316	387	
HCWAR05	932623	759	blastx.14	hypothetical protein [Synechocystis sp.]	gi 1653272 dbj BAA1 8187.1	47% 46% 71%	235 70 321	83 32 301	
HCWB63	667283	782	HMMER 2.1.1	PFAM: Secretory protein of Ysc/FliF family	PF01514	78.2	45	275	
HCWB76	968515	799	HMMER 1.8	PFAM: Helix-loop-helix DNA-binding domain	PF00010	9.77	13	51	
HCWB137	967717	809	blastx.14	URF (pot. 4S protein) [Escherichia coli]	gi 42759 emb CAA25 537.1	63% 85% 60%	9 202 228	179 222 257	
HCWB153	934909	810	blastx.14	lepA [Mycobacterium tuberculosis]	gi 1655655 emb CAB 03723.1	85% 84% 84%	65 9 65	166 5 65	
HCWB190	921653	812	blastx.14	xylose isomerase [Klebsiella pneumoniae]	gi 43952 emb CAA43 389.1	59% 55%	316 344	8 291	
HCWB1N06	924638	825	blastx.14	collagen type XVII [Mus musculus]	gi 309183 gb AAA37 443.1	26% 46%	153 262	266 306	

						57%	5	46
						36%	75	140
						46%	259	303
						43%	310	357
						75%	337	360
						42%	78	119
HCWBQ03	920886	834	blastx.14	ORF YBR208c [Saccharomyces cerevisiae]	gi 536588 emb CAA8 5172.1	42% 54%	147 3	287 74
HCWCM65	529230	891	HMMER 1.8	PFAM: AMP-binding enzymes	PF00501	69.62	31	264
HCWCR31	693632	909	HMMER 2.1.1	PFAM: ATP synthase (E/31 kDa) subunit	PF01991	80	229	381
HCWDI64	924632	945	blastx.14	tetracycline transporter- like protein [Mus musculus]	gi 2506078 dbj BAA2 2622.1	82% 87%	117 73	167 120
HCWDJ23	527555	952	HMMER 2.1.1	PFAM: Bacterial extracellular solute- binding proteins, family 3	PF00497	27.3	25	198
HCWDL45	889416	957	HMMER 1.8	PFAM: Zinc-binding metallopeptidase domain	PF00099	4.63	121	168
HCWDR01	839104	973	HMMER 1.8	PFAM: ABC transporters	PF00005	62.98	15	179
			blastx.2	(AE000411) putative ATP-binding component of a transport system [Escherichia coli]	gb AAC76377.1	69% 44% 51% 41%	9 18 281 391	215 200 373 477
HCWDV17	974478	993	HMMER 1.8	PFAM: Bacterial regulatory proteins, luxR family	PF00196	81.59	416	613
HCwdx22	967361	1014	blastx.14	copC peptide	gi 151190 gb AAA25	79%	365	84

HCwdx76	932614	1019	blastx.14	[Pseudomonas syringae] (AF102543) unknown [Zymomonas mobilis]	808.1  gi 4378174 gb AAD1 9419.1	81% 50% 58% 55%	423 44 9 38	358 232 59 64
HCwed61	971865	1041	blastx.14	gp210 (AA 1-1886) [Rattus norvegicus]	gi 56463 emb CAA68 759.1  PF00099	75%	481	212
HCweg69	948693	1058	HMMER 1.8	PFAM: Zinc-binding metallopeptidase domain		2.79	57	98
HCweI19	948690	1066	HMMER 1.8	orf3 [Pseudomonas aeruginosa]	gi 557259 emb CAA5 7572.1  PF00099	55% 87%	248 56	45 9
HCwel01	916972	1086	blastx.14	formaldehyde dehydrogenase (glutathione) [Escherichia coli]	gi 887431 emb CAA5 2057.1	75%	300	10
HCwem51	920887	1096	blastx.14	(AF010496) exonuclease SbcD homolog [Rhodobacter capsulatus]	gi 3128267 gb AAC1 6119.1	39% 47%	34 193	171 249
HCweQ14	908245	1105	HMMER 1.8	argininosuccinate lyase [Bacillus subtilis]	gi 2635409 emb CAB 14904.1  PF00270	54% 47%	365 57	39 7
HCweW45	571355	1116	HMMER 1.8	PFAM: DEAD and DEAH box helicases	gi 2443870 gb AAB8 1544.1  PF00183	72.08	37	177
HCweY34	954142	1125	blastx.14	(AJ000758) precorrin-4 methylase [Bacillus megaterium]	gi 3724045 emb CAA 04314.1	32%	3	242

HCWFF88	506577	1143	HMMER 1.8	PFAM: Src homology domain 3	PF00018		4.92	140	181
HCWFK57	861907	1149	HMMER 2.1.1	PFAM: RNA polymerase beta subunit	PF00562		36.2	34	270
HCWFT29	690751	1186	HMMER 1.8	PFAM: Helicases conserved C-terminal domain	PF00271		4.51	105	152
HCWFU66	853005	1196	HMMER 2.1.1	PFAM: Aldehyde dehydrogenase family	PF00171		71.4	105	269
HCWGB78	861843	1217	HMMER 2.1.1	PFAM: Ribosomal protein L31	PF01197		50.8	126	236
HCWGE12	967067	1223	HMMER 1.8	PFAM: Bacterial mutT protein	PF00293		4.04	214	288
HCWGW12	964088	1262	blastx.14	L-lactate dehydrogenase (EC 1.1.1.27) - Acinetobacter 1	pir A37334 A37334		73%	137	60
HCWGY90	960159	1288	HMMER 1.8	PFAM: Bacterial regulatory helix-loop- helix proteins, araC family	PF00165		58.7	6	137
			blastx.14	operon regulatory protein [Erwinia carotovora] 811.1	gi 148382 gb AAA24		86%	6	158
HCWHB12	970688	1295	blastx.14	Nodulation protein V (EC 2.7.3.-). [Escherichia coli] 5920.1	gi 1736771 dbj BAAI		4.7% 33% 85%	195 59 310	314 211 330
HCWHD07	953384	1305	blastx.14	Isp42p [Saccharomyces cerevisiae]	gi 736300 emb CAA8 8644.1		41% 46% 50%	56 298 341	301 393 394
HCWHP74	598510	1334	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130		2.09	68	112

HCWHQ03	924187	1336	blastx.14	(AL049608) extensin-like protein [Arabidopsis thaliana]	gi 4584539 emb CAB 40769.1	50% 45% 35% 43% 46% 85% 85%	271 209 300 291 238 14	206 126 253 247 218
HCWHQ31	574945	1337	HMMER 2.1.1	PFAM: Carbon-nitrogen hydrolase	PF00795	39.4	141	308
HCWHR81	935419	1343	HMMER 2.1.1	PFAM: Ribosomal protein L30p/L7e	PF00327	90.5	107	265
HCWHT59	924105	1349	blastx.14	(AF047828) syringomycin synthetase [Pseudomonas syringae pv. syringae]	gi 3510629 gb AAC8 0285.1	57% 45% 50% 50% 36% 34% 61% 55% 40% 33% 66% 55% 26% 26% 44% 41% 41% 33% 22% 57%	261 327 261 261 122 122 329 157 104 107 142 305 249 249 305 157 157 311 107 246 83	148 148 148 148 9 9 252 104 9 9 107 252 160 160 252 107 107 249 15 15 246 27
HCWKF08	959388	1388	blastx.14	pot. ORF I [Homo	gi 1335196 emb CAA	57%		

			sapiens]	26917.1		
HCWKN08	959380	1409	blastx.14	CeoB [Burkholderia cepacia]	gi 2109271 gb AAB58161.1	62% 32% 47%
HCWKV68	959801	1427	blastx.14	(AL121600) hypothetical protein SCF76.09 1	gi 6002364 emb CAB56729.1	55% 50% 62% 54% 34% 42% 57%
HCWL06	935392	1437	blastx.14	ORF_0485 [Escherichia coli]	gi 887832 gb AAA83063.1	169 148 281 61 219 120 238
HCWLE37	960093	1442	blastx.14	(AF039571) peripheral benzodiazepine receptor interacting protein; PBR-IP/PRAX1 [Homo sapiens]	gi 4104812 gb AAD11957.1	100% 85% 87% 44% 36% 35%
HCWLH79	959458	1453	blastx.14	(AC004877) sco-spondin-mucin-like; similar to P98167 1 sapiens]	gi 3638957 gb AAC36301.1	126 304 103 66 250 66
HCWTB11	965024	1462	blastx.14	DNA primase [Escherichia coli]	gi 147755 gb AAA24600.1	263 345 126 119 315 7
HCWTB56	853009	1470	HMMER 1.8	PFAM: E1-E2 ATPases	PF00122	55.15
HCWTB56	853009	1470	HMMER 1.8	cadmium resistance protein [Lactococcus lactis]	gb AAB37345.1	45% 42%
HCWTB56	853009	1470	HMMER 1.8	cadmium resistance protein [Lactococcus lactis]	gb AAB37345.1	341
HCWTR08	958791	1516	blastx.14	(AE000888) malate dehydrogenase	gi 2622314 gb AAB5694.1	66 44%
HCWTR08	958791	1516	blastx.14	[Methanobacterium		134 182

				thermoautotrophicum]				
HCWTR54	729290	1517	HMMER 1.8	PFAM: Helicases conserved C-terminal domain	PF00271		6.14	151
HCWTS15	654317	1519	HMMER 1.8	PFAM: D-isomer specific 2-hydroxyacid dehydrogenases	PF00389	47.52	2	166
HCWUU16	661570	1593	HMMER 1.8	PFAM: Zinc-binding metallopeptidase domain	PF00099	2.17	33	77
HDDMA83	926991	1633	blastx.14	(AF038963) RNA helicase [Homo sapiens] [gb 9826.1 ]	gi 4405795 gb AAD1 9826.1	100% 51% 100% 90%	2 537 656 526	514 635 694 558
HDMAQ15	941282	1646	HMMER 2.1.1	PFAM: POT family	PF00854	7.2	811	386
			blastx.2	(AF121080) cAMP inducible 1 protein [Mus musculus]	gb AAD24570.1 AF1 21080_1	80%	2	997
HDPAG32	947832	1655	HMMER 2.1.1	PFAM: Peptidase family M1	PF01433	39.1	335	577
HDPCN94	794275	1678	HMMER 2.1.1	PFAM: RhoGEF domain	PF00621	54.2	363	740
HDPPF07	974494	1694	blastx.14	(AF151363) Cd42 GTPase-activating protein [Mus musculus]	gi 5020264 gb AAD3 8043.1 AF151363_1	92% 96% 50%	513 715 458	716 789 505
HDPIIT53	926498	1736	blastx.14	(AF109719) BAT2 [Mus musculus]	gi 3941737 gb AAC8 2480.1	50% 30%	229 278	170 219
HDPIIT61.	741724	1737	blastx.2	(AF121080) cAMP inducible 1 protein [Mus musculus]	gb AAD24570.1 AF1 21080_1	73% 57%	48 293	329 397

HDPKD52	959653	1750	HMMER 1.8	PFAM: Fibronectin type III domain	PF00041		4.82	340	402
HDPLC45	909091	1755	HMMER 2.1.1	PFAM: BTB/POZ domain	PF00651		39.5	280	507
HDPMA48	582015	1775	blastx.2	(AF038007) FIC1 [Homo sapiens]	gb AAC63461.1		54%	152	703
HDPMO62	912722	1780	HMMER 1.8	PFAM: Ras family (contains ATP/GTP binding P-loop)	PF00071		132.39	127	432
			blastx.2	rab-related GTP-binding protein [Homo sapiens]	emb CAA68227.1		54% 57%	133 20	444 76
HDPNC96	934520	1788	HMMER 1.8	PFAM: Eukaryotic protein kinase domain	PF00069		206.63	3	734
			blastx.14	HUMAN NDR [unidentified]	gi 2304746 emb CAA 03387.1		92%	3	734
HDPOJ93	792193	1797	HMMER 1.8	PFAM: EF hand	PF00036		7.78	266	313
HDPPP24	812091	1815	HMMER 2.1.1	PFAM: Fes/CIP4 homology domain	PF00611		22.4	151	387
HDPPU44	951276	1818	HMMER 1.8	PFAM: Lectin C-type domain short and long forms	PF00059		37.49	245	376
HDPRH02	919404	1837	blastx.14	ORF YGR090w [Saccharomyces cerevisiae]	gi 1323133 emb CAA 97093.1		30% 48%	266 593	451 673
HDPSG10	961323	1849	blastx.14	reverse transcriptase [Homo sapiens]	gi 439877 gb AAB02 291.1		66% 37% 54%	6 280 235	59 351 267
HDPTW90	722699	1868	HMMER 1.8	PFAM: Ig (immunoglobulin)	PF00047		3.32	1	24

				superfamily				
HDPVG11	966556	1877	HMMER	PFAM: PH (pleckstrin homology) domain	PF00169	16	518	613
HDPWE80	909916	1890	HMMER	PFAM: PH domain	PF00169	81.2	412	708
		2.1.1	blastx.2	(AF102854) membrane-associated guanylate kinase-interacting protein 2 Maguin-2 [Rattus norvegicus]	gb AAD04568.1	36%	349	756
HDPWY46	915964	1894	blastx.14	(AF061738) leucine aminopeptidase [Homo sapiens]	gi 4335941 gb AAD17527.1	94% 87%	3	152 438
						80% 95%	316 254	217 316
						62% 33%	425 305	472 358
HDQEF04	927024	1914	blastx.14	Bassoon [Mus musculus]	gi 3413810 emb CAA76598.1	75%	239	216
HDQGT70	909848	1936	blastx.14	Bat2 [Homo sapiens]	gi 29375 emb CAA78744.1	37%	248	201
HDQHT10	963481	1944	blastx.14	(AF039571) peripheral benzodiazepine receptor interacting protein; PBR-IP/PRAK1 [Homo sapiens]	gi 4104812 gb AAD1957.1	58% 43% 100% 55% 42% 58% 83%	490 387 76 253 256 45 51	455 319 59 227 215 10 34
HDQHZ10	961336	1945	blastx.14	fractionated X-irradiation-induced 29 thymoma [Mus musculus]	gi 1389694 gb AAB02905.1	51% 71%	47 2	256 43
HDQHZ22	879416	1946	blastx.2	cysteine rich hair keratin	emb CAA56339.1	40%	65	319

				associated protein [Oryctolagus cuniculus]		42%	65	352
HDTAY23	973925	1956	blastx.14	(AF086624) serine threonine kinase [Rattus norvegicus]	gi 3800869 gb AAC6 8900.1	98%	78	. 254
HDTAY23	974565	9561	blastx.14	(AF086624) serine threonine kinase [Rattus norvegicus]	gi 3800869 gb AAC6 8900.1	98% 85% 100% 66%	79 330 371 305	255 371 403 331
HDTB048	945083	1959	HMMER 1.8	PFAM: IG (immunoglobulin) superfamily	PF00047	18.53	159	347
			blastx	(AJ009698) embigin protein [Rattus norvegicus]	emb CAA08796.1	58% 75% 58%	132 273 357	248 356 464
HDTBR50	846630	1968	HMMER 1.8	PFAM: Thioredoxins	PF00085	29.85	163	297
HDTBY88	934472	1973	HMMER 2.1.1	PFAM: Eukaryotic protein kinase domain	PF00069	93.6	3	302
			blastx.14	p56 KKIAMRE protein kinase [Homo sapiens]	gi 1517820 gb AAC5 0918.1	82% 35% 100%	3 192 492	170 458 509
HDTDC53	916348	1977	HMMER 1.8	PFAM: Core histones H2A, H2B, H3 and H4	PF00125	7.98	180	233
HDTEI19	912765	1984	blastx.14	rab4b [Canis familiaris]	gi 919 emb CAA3980 0.1			
HDTESS0	964709	1987	HMMER 1.8	PFAM: RNA recognition motif (aka RRM, RBD, or RNP domain)	PF00076	31.58	108	326
			blastx.2	arginine-rich nuclear	gb AAA35554.1	65%	36	350

HDTHQ15	923899	2009	blastx.14	protein [Homo sapiens]	gi 1665781 dbj BAA1 3387.1	97%	4	612
HDTHZ46	957669	2012	blastx.14	Similar to a C.elegans protein encoded in cosmid C27F2 (U40419) [Homo sapiens] (AC004877) spondin-mucin-like; similar to P98167 1 sapiens]	gi 3638957 gb AAC3 6301.1	43% 42% 46% 43% 40% 38%	100 45 172 2 5 318	168 101 216 49 49 371
HDTID61	908946	2016	HMMER 1.8	PFAM: Zinc finger, C2H2 type (AK002053) unnamed protein product [Homo sapiens]	PF00096 dbj BAA92059.1	7.07	407	430
HDTIF01	883070	2017	blastx.2	(AF010144) neuronal -	gb AAC08737.1	61%	315	524





HEOMG48	963338	2091	blastx.14	very large tegument protein [human herpesvirus 2]	gi 1869859 emb CAB06722.1	63% 50% 33% 38% 50% 29%	641 460 338 290 154 82 219	667 428 303 228 92 41 148
HEOMG78	920911	2092	blastx.14	contains similarity to C2 domains [Caenorhabditis elegans]	gi 1825586 gb AAB42222.1	70% 40%	294 136	437 246
HEOMS08	959581	2113	blastx.14	(AF034970) docking protein [Homo sapiens]	gi 3043919 gb AAC13265.1	93% 83%	129 172	173 207
HEOMT79	936687	2118	blastx.14	(AF108420) 1-aminocyclopropane-carboxilate synthase [Fugu rubripes]	gi 4426837 gb AAD20564.1	52%	10	210
HEOMU79	965900	2121	blastx.14	HLA-B-associated transcript 2 (BAT2) [Homo sapiens]	gi 179339 gb AAA35585.1	29%	320	198
HEOMX92	919200	2131	blastx.14	TGR-CCL5bis [Homo sapiens]	gi 1247469 emb CAA01862.1	53% 38% 53% 30%	274 129 271 206	230 91 233 6
HEOMX92	961148	9562	blastx.14	retrovirus-related reverse transcriptase pseudogene - slow loris	pir B25313 GNLRL1	27% 46% 50%	174 206 247	174 241 312
HEONQ19	930705	2142	HMMER 2.1.1	PFAM: PH domain	PF00169	42.5	213	533
			blastx.2	(AJ250425) Collybistin I [Rattus norvegicus]	emb CAB65966.1	96%	9	629

HEONV59	949152	2148	blastx.2	(AK001463) unnamed protein product [Homo sapiens]	dbj BAA91707.1		51% .50%	163 284	279 379
HEOPE58	851009	2157	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099		5.32	320	364
HEOPO08	958184	2174	blastx.14	alpha-1 type II collagen [Xenopus laevis]	gi 214044 gb AAA49 679.1		38% 32% 31% 75% 36%	142 429 429 273 208	11 346 334 250 134
HEOQC76	909032	2189	HMMER 2.1.1	PFAM: Zinc finger, C2H2 type	PF00096		86.9	169	237
			blastx.2	(AK001753) unnamed protein product [Homo sapiens]	dbj BAA91884.1		37% 33% 35% 52% 29%	139 139 139 154 196	609 609 480 306 582
HEOQP44	942596	2203	HMMER 2.1.1	PFAM: Beta-lactamase	PF00144		420.7	250	1026
HEOQS11	965930	2204	blastx.14	ORF1A [Homo sapiens]	gi 475909 emb CAA4 7472.1		51%	30	152
HEORE79	959572	2214	blastx.14	dehydrin [Tortula ruralis]	gi 1732471 gb AAB4 9656.1		53% 46% 50% 50% 55% 42% 62% 62%	101 101 232 284 58 180 223 180	145 145 267 325 84 206 264 203
							62%	302	325

HHECO01	915285	2250	blastx.14	(AF039691) antigen NY-CO-9 [Homo sapiens] 8040.1	gi 3170182 gb AAC1 8040.1	65% 100%	302 25	174 2
HHEEC07	952455	2267	blastx.14	(AF064257) Dhml-like protein [Homo sapiens]	gi 5881961 gb AAD5 5138.1 AF064257.1	99% 100%	1202 1862	1801 1912
HHEHU73	923895	2279	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130	4.1	115	156
HHEJH30	961974	2282	blastx.14	(AF180920) cyclin ania-6a [Homo sapiens]	gi 58223554 gb AAD5 3184.1 AF180920.1	95% 95%	226 429	417 494
HHEND45	919630	2302	HMMER 1.8	PFAM: Double-stranded RNA binding motif blastx.14	PF00035	12.86	25	114
					[D.melanogaster mRNA, complete cds.], gene product [Drosophila melanogaster]	gi 158506 gb AAA73 062.1	52% 47%	114 235 297
HHEQK01	871911	2346	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130	3.27	64	90
HHEQV39	932851	2354	HMMER 1.8	PFAM: Src homology domain 3	PF00018	30.41	526	708
HHESU85	783820	2381	HMMER 1.8	PFAM: Heat shock hsp90 proteins	PF00183	11.81	88	288
HHETQ54	908567	2392	HMMER 2.1.1	PFAM: KRAB box blastx.14	PF01352	166.4	233	421
					NK10 [Mus musculus]	gi 506502 emb CAA5 6225.1	89% 10.48	212 103 186
HHEUA62	965709	2400	HMMER 1.8	PFAM: Spectrin alpha chain, repeated domain blastx.14	PF00435	10.48	103	186
				(AB023622) Septin6 [Mus musculus]	gi 5689158 dbj BAA8 2838.1	59% 60%	13 211	144 315

HHEUC31	795268	2401	HMMER 2.1.1	PFAM: Ank repeat	PF00023		31.5	3	92
HKBAT27	963724	2486	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099		2.17	11	37
HLMBW11	950728	2526	blastx.14 (AF156884) RJP-like kinase [Homo sapiens]	gi 5059425 gb AAD3 9005.1 AF156884_1		92%	129	782	
HLMBY16	531053	2529	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130		1.99	82	123
HLMDU71	531228	2572	HMMER 2.1.1	PFAM: Phosphate-binding protein	PF01449		48.1	1	123
HLMFU09	909666	2600	blastx.14 (AF151363) Cdc42 GTPase-activating protein [Mus musculus]	gi 5020264 gb AAD3 8043.1 AF151363_1		78%	277	372	
HLMHP67	967636	2633	blastx.14	Hypothetical bacteriophage n4 receptor protein NfrA precursor. [Escherichia coli]	gi 1651236 dbj BAA3 5202.1	82% 100%	107 3	340 104	
HLMHHT94	531054	2641	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099		2.86	264	284
HLMIX95	960056	2679	blastx.14 (AB008430) CDEP [Homo sapiens]	gi 2766165 dbj BAA2 4267.1		89% 69%	440 47	330 9	
HLMMAS2	920292	2694	blastx.14	ORF-3 protein [Pseudorabies virus]	gi 334072 gb AAA47 471.1	43% 100% 70%	115 165 174	162 176 203	
HLMMDD05	932127	2697	blastx.14	collagen [Ascaris suum]	gi 159657 gb AAA29 371.1	50% 61% 44% 58% 63% 50%	189 355 189 107 349 387	124 317 115 72 317 352	



							38%	250	197
HLYDS11	966732	2986	blastx.14 [Borna disease virus]	orfIV [Borna disease virus]	gi 473842 gb AAA20 666.1	39%	200	161	3
HLYDT68	526245	2991	HMMER 1.8	PFAM: Zinc finger, C2H2 type	PF00096	4.11	89	124	
HLYDV62	927872	2993	HMMER 2.1.1	PFAM: PH domain blastx.2	PF00169	58.6	188	406	
				(AC005496) unknown protein [Arabidopsis thaliana]	gb AAC35236.1	41% 38%	113 451	292 504	
HLYEN93	682176	3005	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130	2.86	383	409	
HLYGP46	832311	3042	HMMER 2.1.1	PFAM: IQ calmodulin- binding motif	PF00612	24.4	12	74	
HLYHN67	920551	3056	blastx.14	EDTP (egg derived tyrosine phosphatase).	sp BAA33720 BAA3 3720	65% 47%	1 264	234 314	
HMAAF10	968199	3062	blastx.14	Formate c- acetyltransferase (EC 2.3.1.54). [Escherichia coli]	gi 1651427 dbj BAA3 5638.1	100% 76%	1 347	300 385	
HMABJ56	907640	3063	HMMER 2.1.1	PFAM: ADP-ribosylation factor family	PF00025	24.8	157	231	
				blastx.14 (AF082517) ADP- ribosylation factor [Entamoeba histolytica]	gi 3746799 gb AAC6 4063.1	39% 56% 61%	281 154 233	403 228 271	
HMABQ71	729831	3065	HMMER 2.1.1	PFAM: DNA topoisomerase II (N- terminal region)	PF00204	128.8	210	407	

HMADC02	920088	3067	blastx.14	ORF_f418 [Escherichia coli]	gi 536985 gb AA97040.1	95%	202	143
HMADZ55	939916	3071	blastx.2	(AK002022) unnamed protein product [Homo sapiens]	dbj BA92041.1	98%	270	728
HMAFY42	778521	3078	HMMER 2.1.1	PFAM: WH1 domain	PF00568	90	46	303
HMAGK69	723186	3080	HMMER 1.8	PFAM: Signal C terminal domain	PF00512	40.87	31	405
HMAJC22	947905	3085	HMMER 2.1.1	PFAM: Peptidase family M3	PF01432	65.9	115	402
			blastx.14	CG Site No. 18031 [Escherichia coli]	gi 466635 gb AAB18474.1	84% 100% 55%	112 2 363	390 112 422
HMAKA11	966282	9569	blastx.14	MaoB [Escherichia coli]	gi 1480003 dbj BAAl1058.1	99% 90% 50%	1516 1673 1587	803 1545 1474
HMALL66	956195	3091	HMMER 1.8	PFAM: Adenylate kinases	PF00406	50.17	63	296
HMCDN22	895981	3107	blastx.2	(AJ007798) stromal antigen 3, (STAG3) [Homo sapiens]	emb CAB59367.1	82% 90% 71%	85 445 10	456 573 168
HMCFB22	963794	3110	blastx.14	probable transposase - human transposon MER37	pir S72481 S72481	73% 82% 43% 61% 63%	183 119 313 5 90	320 187 423 58 122
HMCGY77	753133	3117	HMMER 2.1.1	PFAM: Kelch motif	PF01344	51.9	7	132
HMMAB49	462502	3127	HMMER	PFAM: Zinc-binding	PF00099	3.49	166	183

HMMAC19	953580	3129	blastx.14 1.8	metalloprotease domain (AF003535) ORF2-like protein [Homo sapiens]	gi 2197085 gb AACD0 46355.1	47% 47%	26 282	145 344
HMMCH04	944069	3208	blastx.2 1.8	unknown [Homo sapiens] PFAM: Helix-loop-helix DNA-binding domain	gb AAC50940.1  PF00010	87% 58%	187 423	210 680
HMQBU96	765162	3247	HMMER 1.8	urokinase plasminogen activator receptor [Homo sapiens]	gi 433901 emb CAA5 2191.1	100% 91%	89 133	8 124
HMQDZ19	940694	3267	blastx.14 1.8	YKL249 [Saccharomyces cerevisiae]	gi 871536 emb CAA4 9304.1	92% 51% 50%	260 141 323	108 1 282
HMSBV28	970579	3303	blastx.14 1.8	PFAM: Src homology domain 3	PF00018	41.06	453	599
HMSCD15	918133	3310	HMMER 1.8	AK000975) unnamed protein product [Homo sapiens]	dbj BAA91451.1	98% 29% 28%	453 387 80	635 479 175
HMSFR69	738588	3373	HMMER 1.8	PFAM: Core histones H2A, H2B, H3 and H4	PF00125	7.78	258	202
HMSGI27	855759	9573	HMMER 1.8	PFAM: Bacterial mutT protein	PF00293	5.56	276	202
HMSGP73	925385	3401	blastx.14 1.8	(AC004490) R29381_1 [Homo sapiens]	gi 2995577 gb AAC0 8316.1	94% 95%	141 901	908 972
HMSGX14	871492	3413	HMMER 1.8	PFAM: Ribosomal protein S12	PF00164	33.44	28	153
HMSHO64	746582	3431	HMMER 1.8	PFAM: Src homology domain 3	PF00018	11.08	316	405
			blastx.2 1.8	(AF030131) Plenty of SH3s; POSH [Mus]	gb AAC40070.1	47%	1	411

HMSHZ56	733386	3447	HMMER 1.8	PFAM: Zinc finger, CCHC class	PF00098		4.89	208	228
HMSJT11	965007	3491	blastx.14	(AF148805) latent nuclear antigen [Kaposi's sarcoma- associated herpesvirus]	gi 5669894 gb AAD4 6501.1 AF148805_6	20% 24% 21% 23% 16%	667 241 241 211 139	1137 465 465 453 465	
HMSJW19	744990	3498	HMMER 2.1.1	PFAM: BAH domain	PF01426		48.7	2	163
HMSKI08	959413	3509	blastx.14	(AF094516) E1-like protein [Homo sapiens]	gi 3820614 gb AAC6 9630.1	97%	97	513	
HMSOM08	958216	3538	blastx.14	(AF082556) TRF1- interacting ankyrin-related ADP-ribose polymerase	gi 3929219 gb AAC7 9841.1	76%	2	232	
HMSOU92	948130	9578	blastx.2	(AF118082) PRO1902 [Homo sapiens]	gb AAF22026.1 AF1 18094_21	64% 63% 88%	302 462 532	463 527 558	
HMSOX47	948202	3548	blastx.14	cDNA EST EMBL:M89462 comes from this gene; cDNA EST 11 yk349d7.5 comes from this gene; cDNA EST yk358b9.5 comes from this	gi 3879085 emb CAA 94301.1	48% 39% 36% 39% 26%	514 365 266 173 514	612 463 355 256 591	
HMVVDU16	904807	3589	HMMER 1.8	PFAM: Core histones H2A, H2B, H3 and H4	PF00125		13.38	1252	1329
HMWCQ09	924634	3606	blastx.14	Emf1 alpha [Ephydium muelleri]	gi 9300 emb CAA494 72.1	50% 33% 66%	19 99 217	84 233 243	

HMWDD54	932261	3610	blastx.14	(AF175223) SANT domain protein SMRTER [Drosophila melanogaster]	gi 5815245 gb AAD52614.1 AF175223_1	38%	292	345
HMWDF88	906769	3612	HMMER 1.8	PFAM: Low-density lipoprotein receptor domain class A	PF00057	41.61	171	245
			blastx.14	(AF110520) NG29 [Mus musculus]	gi 4050096 gb AAC97969.1	69% 48% 35% 50%	114 129 9 72	239 239 110 107
HMWGG55	920575	3642	blastx.14	DNA polymerase [Pyrococcus furiosus]	gi 216918 db BAA02362.1	94%	195	308
HMWGT07	953454	3645	blastx.14	(AL078579) putative protein [Arabidopsis thaliana]	gi 4972120 emb CAB4397.1	40% 40% 46%	218 395 113	322 475 157
HMWHN70	851334	3654	HMMER 1.8	PFAM: Zinc finger, C3HC4 type (RING finger)	PF00097	6.51	187	255
HNEBJ08	958742	3689	blastx.14	mucin 2 precursor, intestinal - human (fragments)	pir A49963 A43932	35% 83%	305 320	264 303
HNEDU01	909832	3748	blastx.14	(AC002398) F25965_3 [Homo sapiens]	gi 2477513 gb AAB81198.1	71% 57% 62% 43% 50%	207 80 1 323 337	323 205 87 412 384
HNEEF95	971171	3792	blastx.14	ORF_9493 [Escherichia coli]	gi 606260 gb AAA58123.1	98% 89% 81%	548 103 185	201 20 105
HNFFM25	705856	3818	HMMER	PFAM: Laminin B	PF00052	0.47	520	603

			1.8	(Domain IV)				
HNFFT62	574623	3828	HMMER 1.8	PFAM: C2 domain	PF00168		2.74	207
HNFGI01	921431	3851	blastx.14	(AF118890) s-tomosyn isoform [Rattus norvegicus]	gi 4689231 gb AAD2_7819_1 AF118890_1	86% 100% 40%	234 153 287	302 200 361
HNFGI49	909707	3852	blastx.14	(AF086624) serine/threonine kinase [Rattus norvegicus]	gi 3800869 gb AAC6_8900_1	100% 100%	1 60	45 86
HNFGM76	908665	3862	HMMER 2.1.1	PFAM: Zinc finger, C2H2 type	PF00096	74.8	232	306
			blastx.2	(AF132599) RANTES factor of late activated T lymphocytes-1 [Homo sapiens]	gb AAD26864_1 AF1_32599_1	92%	1	417
HNFHA11	967520	3874	HMMER 2.1.1	PFAM: Phosphoenolpyruvate carboxykinase	PF01293	118.1	55	219
			blastx.14	phosphoenolpyruvate carboxykinase [Escherichia coli]	gi 606337 gb AAA58_200_1	99%	55	360
HNFHK77	576186	3890	HMMER 2.1.1	PFAM: Aldehyde dehydrogenase family	PF00171	30.2	231	326
HNFHQ01	938114	3897	blastx.14	serine/threonine kinase with SH3 domain, leucine 1	gi 758593 emb CAA8_8531_1	28% 46% 46% 25% 41%	248 43 371 79 176	331 81 415 186 211
HNFHW14	939763	3908	HMMER 2.1.1	PFAM: Latrophilin/CL-1-like GPS domain	PF01825	35.1	44	196

		blastx.2	(AF166382) serpentine receptor [Mus musculus].	gb AAF00617.1 AF1 66382_1	44%	38	283
HNF07	918389	3921	blastx.14 (AF128881) PI3 kinase regulatory subunit P101	gi 4928058 gb AAD3 3397.1 AF128881_1	80% 60%	2 448	445 477
HNFIP50	965283	3936	blastx.14 mutant sterol regulatory element binding protein-2	gi 841318 gb AAA85 718.1	65% 34% 85%	356 42 665	631 128 685
HNGAL92	953889	3976	blastx.14 phosphatidylserine decarboxylase	gi 551827 gb AAA83 896.1	73%	212	18
HNGAS51	773208	3984	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	2.57	144	182
HNGBF80	574475	4001	HMMER 1.8	PFAM: Zinc finger, C2H2 type	4.98	88	111
HNGBH77	577361	4005	HMMER 1.8	PFAM: ATP synthase A chain	9.81	130	189
HNGCE85	970738	4039	blastx.14	hypothetical protein Tigger 2 - human transposon MER37 1	72% 63%	284 212	210 180
HNGCX07	953900	4065	HMMER 1.8	PFAM: Src homology domain 3	3.68	45	161
HNGEN37	663955	4160	HMMER 2.1.1	PFAM: Indole-3-glycerol phosphate synthases	125.4	2	223
HNGEQ07	953647	4169	HMMER 1.8	PFAM: TPR Domain	PF00515	10.86	164
HNGER43	699391	4173	HMMER 1.8	PFAM: Bacterial mutT protein	PF00293	3.79	151
HNGER96	922996	4177	blastx.14	Bkm-like protein [Drosophila melanogaster]	gi 552132 gb AAA28 872.1	60% 64%	250 250
							294 291

							64%	250	291
							75%	215	250
							80%	28	57
							4.66	194	247
HNGEW76	572874	4198	HMMER 1.8	PFAM: Helicases conserved C-terminal domain	PF00271				
HNGEX35	959230	4200	blastx.14	adenine phosphoribosyltransferase [Escherichia coli]	gi 1773151 gb AAB4 0223.1		98%	205	366
HNGEX95	572897	4202	HMMER 1.8	PFAM: Zinc finger, C2H2 type	PF00096		5.32	196	219
HNGFG22	573084	4224	HMMER 1.8	PFAM: Bacterial regulatory proteins, LuxR family	PF00196		9.2	166	240
HNGFG69	926873	4227	blastx.14	collagen [Ascaris suum]	gi 159657 gb AAA29 371.1		44%	228	175
							40%	145	80
							40%	145	80
							40%	307	248
							50%	67	38
HNGFK28	544726	4234	HMMER 1.8	PFAM: ABC transporters	PF00005		86.07	445	654
			blastx.2	MsbA protein. [Escherichia coli]	dbj BAA35658.1		100%	1	651
							86%	654	989
HNGFK28	566798	9584	HMMER 1.8	PFAM: ABC transporters	PF00005		86.07	445	654
			blastx.2	MsbA protein. [Escherichia coli]	dbj BAA35658.1		100%	1	651
							100%	654	989
HNGFK28	943114	9585	HMMER 1.8	PFAM: ABC transporters	PF00005		117.67	342	1
			blastx.2	MsbA protein.	dbj BAA35658.1		100%	165	503

			[Escherichia coli]			84% 91%	2.5 2	162 37
HNGFK28	943115	9586	HMMER 2.1.1	PFAM: ABC transporter transmembrane region.	PF00664	60.9	3	242
			blastx.2	MsbA protein. [Escherichia coli]	dbj BAA35658.1	99%	3	512
HNGFO46	935135	4244	blastx.14	hypothetical protein T23G.2 - Caenorhabditis elegans	pir S28303 S28303	44% 60% 40% 36%	84 116 205 263	10 87 161 198
HNGFO81	526792	4246	HMMER 2.1.1	PFAM: Integrase core domain	PF00665	42.7	84	215
HNGFUI2	971170	4265	HMMER 1.8	PFAM: RNase H	PF00075	55.68	102	290
			blastx.14	reverse transcriptase (476 AA) [Woolly monkey sarcoma virus]	gi 930259 emb CAA3 3367.1	44% 60%	96 1	422 75
HNGFW09	924693	4270	blastx.14	180 kDa bullous pemphigoid antigen 2/type XVII collagen [Homo sapiens]	gi 1877435 gb AABS 1499.1	50% 53% 66% 36% 75% 85% 85% 60% 54% 50%	196 167 155 75 152 152 152 335 196 289	155 129 129 1 129 132 132 306 167 164 248

						75% 66% 66% 60%	152 155 155 193	129 129 129 164
HNGGH78	924908	4306	blastx.14	type VII collagen [Cricetulus griseus]	gi 388625 gb AAA36 968.1	50% 34% 42% 40% 50% 58% 38% 41% 50%	356 47 285 288 171 171 6 53 171	397 115 341 347 206 206 59 103 206
HNGGM10	964819	4317	HMMER 1.8	PFAM: Laminin B (Domain IV)	PF00052	0.51	424	441
HNGGR74	765698	4340	HMMER 1.8	PFAM: Zinc finger, C2H2 type	PF00096	6.36	14	58
HNGHT06	935706	4450	blastx.14	unknown protein [Homo sapiens]	gi 1196398 gb AAA8 8020.1	50%	254	177
HNGIJ01	916748	4483	blastx.14	ORF2 [Rattus norvegicus]	gi 56588 emb CAA37 645.1	50% 57% 57%	168 280 73	293 342 114
HNGKE07	952221	4630	blastx.14	collagen type VII [Homo sapiens]	gi 495866 gb AAA58 965.1	58% 55% 47% 64% 57% 32% 33% 62%	336 93 155 155 327 266 87 81	286 40 105 327 286 225 13 1
HNGLE52	835972	4662	HMMER	PFAM:	PF00049	6.75	286	318

			1.8	Insulin/IGF/Relaxin family				
HNGLG06	839088	4666	HMMER 1.8	PFAM: ABC transporters	PF00005	47.92	348	599
			blastx.2	Hypothetical protein HJ0658 [Escherichia coli]	dbj BAA35501.1	99% 38%	270 288	665 569
HNGLH82	954140	4668	blastx.14	diaminopimelate decarboxylase [Escherichia coli]	gi 455170 gb AAA83 861.1	98% 71% 63%	416 193 258	249 47 136
HNGMM87	806036	4715	HMMER 1.8	PFAM: ATP synthase A chain	PF00119	8.41	237	362
HNGOO22	953888	4762	blastx.14	(AE000449) putative xylose [Escherichia coli]	gi 1790156 gb AAC7 6742.1	94% 91%	104 151	3 116
HNHAII1	967668	4790	blastx.14	p15E carboxyterminal sequence [Kirsten murine sarcoma virus]	gi 4469304 emb CAA 25493.1	38% 28% 53%	262 406 310	161 323 272
HNHB19	724404	4798	HMMER 1.8	PFAM: Helicases conserved C-terminal domain	PF00271	4.4	113	145
HNHY45	774280	4823	HMMER 1.8	PFAM: ATP synthase A chain	PF00119	8.4	228	347
HNHDY74	506621	4878	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130	1.89	395	427
HNHDY50	924211	4910	blastx.14	unknown protein [Homo sapiens]	gi 1196398 gb AAA8 8020.1	50% 44% 41%	33 23 6	170 169 164
HNHEJ85	964882	4955	blastx.14	synexin - bovine (fragment)	pir A27695 A27695	54% 46%	47 91	15 53

HNHET2S	953410	5002	blastx.14	(AJ005562) SPR2D protein [Mus musculus]	gi 3093363 emb CAA06591.1		40% 38%	114 91	85 53
HNHFA11	967126	5030	blastx.14	(AF144054) apoptosis related protein APR-4 [Homo sapiens]	gi 4868437 gb AAD31316.1 AF144054_1		32% 43% 46%	347 250 207	246 203 169
HNHGD07	953416	5121	blastx.14	(AF053091) eyelid [Drosophila melanogaster]	gi 2981221 gb AAC06254.1		52% 35%	212 342	355 401
							46% 55% 33% 30% 50% 36% 26% 62% 42% 62% 83%	164 227 295 259 346 268 259 367 322 367 367	241 280 384 384 381 333 384 390 378 390 384
HNHGEO9	939727	5127	blastx.2	IDN4-GGTR14 PROTEIN.	sp Q9Y6Y5 Q9Y6Y5	81%	2	112	
HNHGH20	959499	5146	blastx.14	notch4 [Homo sapiens]	gi 1841543 gb AAC63097.1	43% 77% 33% 33% 62%	56 154 256 297 131	9 128 167 244 108	
HNHGV22	674653	5189	HMMER 1.8	PFAM: Helicases conserved C-terminal domain	PF00271	4.66	94	138	
HNHHI10	964659	5251	blastx.14	ORF1 [Rattus norvegicus]	gi 56587 emb CAA37644.1	56% 34%	75 157	28 71	

							33% 63%	220 187	158 155
HNHHL74	765598	5266	HMMER 1.8	PFAM: Bacterial mutT protein	PF00293		3.57	83	148
HNHIA95	908419	5318	HMMER 2.1.1	PFAM: gag gene protein p24 (core nucleocapsid protein)	PF00607		67.6	49	300
HNHPH29	934456	5496	blastx.14	(AF118275) atrophin- related protein ARP [Homo sapiens]	gi 4680231 gb AAD2 7584.1 AF118275_1		60% 45% 70% 50% 47%	363 14 91 262 310	407 73 120 297 360
HOIAE91	9353222	5497	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130		2.66	200	235
HSATQ28	866951	5512	HMMER 1.8	PFAM: Ubiquitin carboxyl-terminal hydrolases family 2	PF00442		11.1	90	122
HSAYN79	471037	5646	HMMER 1.8	PFAM: RNA recognition motif. (aka RRM, RBD, or RNP domain)	PF00076		4.12	360	380
HSYBL15	660053	5682	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130		22.31	2	70
HSYDP04	970789	5686	blastx.14	(AF113615) FH1/FH2 domain-containing protein FHOS [Homo sapiens]	gi 5106956 gb AAD3 9906.1 AF113615_1		100% 50% 47%	77 408 393	394 467 443
HT3SA07	954360	5702	blastx.14	ORF2 contains a reverse transcriptase domain.; ORF2 [Homo sapiens]	gi 339771 gb AAAS1 622.1		50% 54%	83 47	178 79
HT4GJ85	909971	5714	HMMER	PFAM: PH (pleckstrin	PF00169		11.11	365	451

		blastx.14 1.8	homology domain				
		(AF053974) SWAP-70 [Mus musculus]	gi 3290154 gb AAC4 0155.1	53% 88%	251 4	448 4	448 54
HTSEA69	952359	5721	blastx.14 (AL032624) cDNA EST yk321h8.5 comes from this gene; 1 from this gene [Caenorhabditis elegans]	gi 3881086 emb CAA 21522.1	33% 30%	448 123	492 251
HTAAW46	719422	5735	HMMER 1.8	PFAM: HMG (high mobility group) box	PF00505	5.82	6
HTABG87	940153	5745	HMMER 1.8	PFAM: Eukaryotic protein kinase domain	PF00069	13.81	240
			blastx.14 1.8	(AF006064) protein kinase homolog [Fowlpox virus]	gi 2393890 gb AAC5 8236.1	54% 33%	8 189
HTACW17	961560	5760	blastx.14 1.8	(AC007660) unknown protein [Arabidopsis thaliana]	gi 4895220 gb AAD3 2806.1 AC007660_7	37% 61%	139 212
HTAFE69	944409	5797	blastx.2 2.1.1	(AK000496) unnamed protein product [Homo sapiens]	dbj BAA91205.1	356 265	356 265
HTAHL45	908949	5817	HMMER 2.1.1	PFAM: SCAN domain	PF02023	69%	432
			blastx.14 2.1.1	(AC004522) Zn-finger- like protein; similar to Z98745 (PID:22924250) [Homo sapiens]	gi 3006231 gb AAC0 9486.1	228.7	704
HTAHV04	926747	5826	blastx.14 2.1.1	(AC005757) R32611_1 [Homo sapiens]	gi 3688089 gb AAC6 2258.1	100% 3	446 3
HTAJN08	958057	5841	HMMER	PFAM: Helicases	PF00271	5.49	20
						55	55

		1.8	conserved C-terminal domain				
HTDAE43	971582	9597	blastx.14 (AF144054) apoptosis related protein APR-4 [Homo sapiens]	gi 4868437 gb AAD3 13161 AF144054_1	53%	526	296
HTGCH58	909849	5895	HMMER 2.1.1 blastx.14	PFAM: RhoGAP domain carboxyl terminus of the predicted protein shows 1 1 comes from this gene; cDNA EST EMBL:D32994 comes from this gen	PF00620 gi 3874826 emb CAA 86318.1	91.4 44% 61%	420 657 771
HTGDM65	967158	5918	blastx.14	SH3 domain binding protein [Rattus norvegicus]	gi 1185397 gb AAA8 7791.1	39% 50% 39% 47% 39% 28% 40%	127 186 278 186 278 337 260
HTGDT91	974962	5921	HMMER 2.1.1 blastx.14	PFAM: SpoU rRNA Methylase family alternate gene name yibK [Escherichia coli]	PF00588 gi 466744 gb AAB18 583.1	107.6 100% 100% 76% 81%	315 315 531 457 497
HTGDW96	967030	5926	HMMER 2.1.1 blastx.14	PFAM: Domain of unknown function (AL034490) similar to yeast ngl-1-interacting factor 3	PF01784 gi 4008560 emb CAA 22481.1	130.2 60% 43% 37%	334 1087 460 385
						711	1275 660 513

			[Schizosaccharomyces pombe]			61%	361	414
						28%	970	1065
						58%	1312	1347
HTGEL46	685425	5936	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130	7.26	398	433
HTGEQ11	967047	5944	HMMER 2.1.1	PFAM: Cytosol aminopeptidase family	PF00883	191	27	305
			blastx.14	aminopeptidase A [Escherichia coli]	gi 1054725 emb CAA60164.1	95% 83% 88%	27 320 1	305 391 27
HTGER72	683469	5949	HMMER 1.8	PFAM: Src homology domain 3	PF00018	2.4	174	203
HTGFZ03	923443	5968	HMMER 2.1.1	PFAM: RNA polymerase beta subunit	PF00562	30.7	21	110
			blastx.14	(AF025424) RNA polymerase I 127 kDa subunit [Rattus norvegicus]	gi 2739048 gb AAB94600.1	76%	3	275
HTGGL23	974590	5973	blastx.14	(AE000218) putative adhesion and penetration protein [Escherichia coli]	gi 1787452 gb AAC74286.1	87%	3	443
HTHCB68	660309	5996	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	3	162	209
HTJAB35	880424	9601	HMMER 1.8	PFAM: Ank repeat	PF00023	35.64	242	325
HTJMT23	948518	6056	blastx.14	(AF182426) arylacetamide deacetylase [Rattus norvegicus]	gi 5923874 gb AADS6394.1 AF182426_1	58%	2	160
HTOAK34	966800	6081	HMMER	PFAM: Eukaryotic protein	PF00069	32.41	1020	1190

		1.8 blastx.14	kinase domain (AF084205) serine/threonine protein kinase TAO1 [Rattus norvegicus]	gi 3452473 gb AAC7 1014.1		75%	954	1190
HTODG16	909952	6108 HMMER 2.1.1	PFAM: RasGEF domain	PF00617		148.5	4	402
HTOFT34	527144	6146 HMMER 1.8	CDC25 [Saccharomyces kluyveri] PFAM: Phorbol esters / diacylglycerol binding domain	gi 171187 gb AAA34 479.1  PF00130		4.53	235	264
HTOHL35	537364	6173 HMMER 1.8	PFAM: Zinc finger, C2H2 type	PF00096		6.52	4	33
HTOIY09	836003	6201 HMMER 1.8	PFAM: Insulin/MGF/Relaxin family	PF00049		7.08	61	123
HTSHF47	720403	6229 HMMER 1.8	PFAM: Helix-loop-helix DNA-binding domain	PF00010		7.82	105	140
HTSHM38	972248	6230 HMMER 2.1.1	PFAM: EGF-like domain	PF00008		72	299	406
			(AB011532) MEGF6 [Rattus norvegicus]	gi 3449294 dbj BAA3 2462.1		88% 50% 53% 42% 43% 40% 46% 70% 66%	287 278 320 299 287 290 341 287 114	538 460 466 460 442 427 481 415 173 413 457

50%	467	532
61%	245	283
35%	188	280
47%	482	538
52%	245	295
39%	476	544
61%	245	283
55%	230	283
31%	188	283
50%	245	286
29%	170	280
69%	245	283
53%	245	283
50%	485	532
35%	452	535
47%	482	532
47%	482	532
50%	245	304
31%	299	412
70%	251	280
58%	251	286
30%	434	532
58%	245	280
53%	245	283
37%	245	316
63%	317	349
75%	245	268
47%	245	295
37%	251	322
54%	251	283
31%	320	406

36%	230	286
40%	401	460
60%	203	232
54%	473	505
34%	308	376
50%	245	280
25%	329	445
62%	245	268
37%	485	532
29%	251	343
50%	227	262
45%	251	283
24%	296	406
71%	485	505
40%	473	532
33%	344	406
71%	359	379
50%	245	280
60%	454	483
62%	245	268
33%	491	544
33%	320	382
63%	344	376
62%	359	382
71%	203	223
45%	203	235
37%	215	262
37%	359	406
38%	356	409
36%	320	376
40%	320	379

HTWCG65	869547	6260	HMMER 1.8	PFAM: Core histones H2A, H2B, H3 and H4	PF00125		60%	251	280
HTWEY30	918641	6299	blastx.14	(AF036548) RGC-32 [Rattus norvegicus]	gi 3800742 gb AAC6 8839.1		88%	613	434
HTWJA59	812705	6314	HMMER 1.8	PFAM: Helicases conserved C-terminal domain	PF00271		4.95	172	219
HTXCY84	924996	6359	HMMER 2.1.1	PFAM: Aldehyde dehydrogenase family blastx.14	PF00171		23.9	104	217
				(AF038838) proline dehydrogenase [Klebsiella aerogenes]	gi 2766693 gb AAB9 5478.1		78% 45% 41%	47 16 20	241 48 70
HTXDW14	966588	6366	blastx.14	(AB029335) HRPET-3 [Halocynthia roretzii]	gi 5360271 dbj BAA8 1908.1		54% 45%	869 773	777 663
HTXDX61	784768	6367	HMMER 2.1.1	PFAM: Amidase	PF01425		123.2	61	330
HTXFN69	869397	6394	HMMER 1.8	PFAM: HMG (high mobility group) box	PF00505		6.76	72	137
HTXGL73	529745	6403	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130		2.21	144	176
HTXJL68	912611	6420	blastx.14	RAB14 [Rattus norvegicus]	gi 206535 gb AAA41 994.1		97% 60% 59% 52%	230 367 482 373	370 450 547 429
HTXJM73	783572	6425	HMMER 1.8	PFAM: Bacterial mutT protein	PF00293		2.87	97	123
HTXKQ55	947789	6453	HMMER 2.1.1	PFAM: Peptidase family M3	PF01432		50.1	3	299

		blastx.14	mitochondrial intermediate peptidase precursor [Homo sapiens]	gi 1763642 gb AAC5 1231.1	96% 100%	3 335	302 367
HTXNY74	918076	6525	blastx.14 (AF078856) p47 [Homo sapiens]	gi 5531827 gb AAD4 4488.1	89% 96%	93 2	530 94
HTXPPT68	870074	6555	HMMER 2.1.1	PFAM: NOL1/NOP2/sun family	PF01189	43.1	29 196
HTXQC36	961161	6560	blastx.14 [Canis familiaris]	(AB012223) ORF2 [Canis familiaris]	gi 2981631 gb BAA2 5253.1	51% 57% 60% 42%	9 326 145 170
HTXRMM86	975072	6575	HMMER 2.1.1	PFAM: Prokaryotic DNA topoisomerase	PF01131	99	243 446
			blastx.14 [Escherichia coli]	DNA topoisomerase III (EC 5.99.1.-) [Escherichia coli]	gi 742870 gb BAA1 5551.1	51% 40%	177 3
HTXSB88	914627	6577	blastx.14 [Homo sapiens]	(AF077042) 30S ribosomal protein S7 homolog [Homo sapiens]	gi 4689132 gb AAD2 7775.1 AF077042_1	84%	559 771
HTXSR92	973095	6579	blastx.2 [Rattus norvegicus]	(AB016962) synGAP-b1 [Rattus norvegicus]	dbj BAA74972.1	60% 55%	302 1
HUJAM39	911399	6586	blastx.14 [Homo sapiens]	(AF051325) SH3 domain containing adaptor protein [Homo sapiens]	gi 4091782 gb AAC9 9298.1	46% 32%	170 709
HUJCM08	957784	6589	blastx.14 [Homo sapiens]	(AF015950) telomerase reverse transcriptase [Homo sapiens]	gi 2330017 gb AAC5 1672.1	100%	2
HUJUAV06	966816	6597	blastx.14 [Homo sapiens]	(AF151854) CGI-96 protein [Homo sapiens]	gi 4929661 gb AAD3 4091.1 AF151854_1	88% 100% 68% 36%	595 464 537 561

HWAAF66	908541	6612	HMMER 2.1.1	PFAM: KRAB box	PF01352		65.3	90	278
		blastx.14	repressor protein [Homo sapiens]	gi 2789430 dbj BAA24380.1		54%	60	212	
HWAAY03	923734	6619	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130		2.21	332	373
HWACA38	943074	6637	HMMER 1.8	PFAM: Bacterial mutT protein	PF00293		3.68	344	376
		blastx.14	(AL033536) predicted using Genefinder; similar to <i>C. elegans</i>	gi 3947651 emb CAA22138.1		39% 52%	251 766	433 834	
HWADF26	957347	6656	HMMER 1.8	PFAM: Lectin C-type domain short and long forms	PF00059		104.26	859	509
		blastx.2	(AF175206) lectin-like receptor F1 [Homo sapiens]	gb AAF37804.1 AF175206_1		100%	3	596	
HWAEN20	868490	6691	HMMER 1.8	PFAM: Zinc finger, C2H2 type	PF00096		6.01	251	313
HWAFW39	947915	6697	HMMER 2.1.1	PFAM: Peptidase family M1	PF01433		79.5	200	367
		blastx.2	(AF106037) adipocyte-derived leucine aminopeptidase [Homo sapiens]	gb AAF07395.1 AF106037_1		96%	200	367	
HWAFX39	907631	6698	blastx.14	Zn-binding protein [Pleurodeles waltl]	gi 213868 gb AAA49614.1	46% 50%	118 19	354 120	
HWAGM33	888685	6710	HMMER 2.1.1	PFAM: Plexin repeat	PF01437		25.8	898	1035

HWAGX37	959586	6711	blastx.14	unknown protein [Homo sapiens]	gi 1196433 gb AAA8 8038.1		47% 34% 42% 29%	215 535 409 295	283 639 471 396
HWAHI10	960646	6714	blastx.14	retinoid X receptor interacting protein [Mus musculus]	gi 709961 gb AAC52 167.1		62% 66% 45% 44%	1215 513 642 1272	583 343 412 1198
HWAHS94	909667	6715	blastx.14	(AF151363) Cdc42 GTPase-activating protein [Mus musculus]	gi 5020264 gb AAD3 8043.1 AF151363_1		66% 63% 75%	1824 278 487	1798 484 510
HWBAL44	959449	6720	blastx.14	(AF151877) CGI-119 protein [Homo sapiens]	gi 4929707 gb AAD3 4114.1 AF151877_1	100%	531	424	
HWBAQ16	868363	6722	HMMER	PFAM: RNA recognition motif. (aka RRM, RBD, or RNP domain)	PF00076		4.8	857	898
HWBBR65	747723	6741	HMMER	PFAM: Zinc-binding metalloprotease domain	PF00099		4.15	185	205
HWBDM24	963498	6771	blastx.14	(AJ388555) hypothetical protein [Canis familiaris]	gi 5441611 emb CAB 46854.1	83% 100% 88%	908 990 837	997 1040 863	
HWBEX27	682583	6785	HMMER	PFAM: Helix-loop-helix DNA-binding domain	PF00010		38.64	184	336
HYAAF33	915050	6820	blastx.14	(AF121858) sorting nexin 8 [Homo sapiens]	gi 4689256 gb AAD2 7831.1 AF121858_1	81% 96% 36%	273 217 172	434 306 270	
HYAAS08	926017	6831	blastx.14	ORF-3 protein [Pseudorabies virus]	gi 334072 gb AAA47 471.1	62% 34% 36% 63%	203 84 125 150	156 7 69 118	

HYABP53	971448	6848	HMMER 2.1.1	PFAM: Immunoglobulin domain	PF00047		37%	282	211
HYABB43	800006	6860	HMMER 2.1.1	PFAM: Alpha-2- macroglobulin family alpha-2-macroglobulin [Mus musculus]	PF00207	90.9	206	257	427
HYAAU65	909956	6863	HMMER 2.1.1	PFAM: RasGEF domain	gb AAA39508.1	67%	263	36	
HWBEG18	909798	6883	HMMER 2.1.1	PFAM: EF hand	PF00617		47	2	112
				(AF106071) ras activator RasGRP [Homo sapiens]	gi 4038292 gb AAC9 7349.1	71% 59% 46% 70% 48% 66%	698 382 103 604 2 619	889 597 420 684 2 654	
HWBCS08	909031	6897	HMMER 2.1.1	PFAM: B-box zinc finger.	PF00643	32.5	263	388	
				(AF119043) transcriptional intermediary factor 1 gamma; TIF1gamma [Homo sapiens]	gi 4325109 gb AAD1 7259.1	92%	2	562	
HWBAQ71	944080	6918	blastx.2	predicted using Genefinder [Caenorhabditis elegans]	emb CAA97423.1	34%	141	464	
HWAFG12	969605	6934	blastx.14	(AF071081) proline-rich mucin homolog [Mycobacterium tuberculosis]	gi 5305335 gb AAD4 1594.1 AF071081_1	34% 50% 28% 40%	112 195 398 365	17 142 264 300	



HWAEC08	958115	6947	HMMER 2.1.1	PFAM: Spectrin repeat [Homo sapiens] blastx.14	norvegicus PF00435 gi 5262574 emb CAB 45729.1	29.5	3	215
HWACY70	756888	6956	HMMER 2.1.1	PFAM: RIO1/ZK632.3/MJ0444 family	PF01163 PF01182 unnamed protein product [unidentified]	96 225.7	280	552
HWABG11	949088	6971	HMMER 2.1.1	PFAM: Glucosamine-6- phosphate isomerase	emb CAA03416.1  similar to SH3-binding protein [Homo sapiens] blastx.2	91% 82% 100% 77% 100%	67	381
HUUDR34	944903	6984	blastx.14	gi 4826478 emb CAB 42896.1	91% 82% 100% 77% 100%	67	480	550
HUUCJ02	940813	6986	blastx.14	(AF132984) nuclear pore complex interacting protein NPIP [Homo sapiens]	gi 4959568 gb AAD3 4394.1 AF132984_1 99% 89% 71% 58% 87% 100% 54% 60% 81% 83% 40% 100% 90%	770 417 250 300 226 278 231 261 226 261 196 258 199 181 152 149 152 126 192	417 250 187 119 231 226 117 149 149 126 163	417 250 187 119 231 226 117 149 149 126 163

HTXOO15	869261	7011	HMMER 2.1.1	PFAM: Ubiquitin family	PF00240		66%	300	274
HTXLS08	958357	7023	blastx.14	(AF090989) high-risk human papilloma viruses E6 1 alpha [Homo sapiens]	gi 4151328 gb AAD1 2543.1	48% 68% 41% 57% 70% 27%	745 1006 1 511 427 580	130	273
HTWKB07	952841	7085	blastx.14	(AF003535) ORF2-like protein [Homo sapiens]	gi 2197085 gb AAD0 4635.1	60% 75% 50% 33% 36% 70%	25 259 205 258 116 167	84 294 205 258 116 196	
HTWJH08	790185	7087	blastx.2	(AK000385) unnamed protein product [Homo sapiens]	dbj BAA91131.1	61%	197	51	
HTWJH08	846554	9615	blastx.2	(AK000385) unnamed protein product [Homo sapiens]	dbj BAA91131.1	61%	197	51	
HTWFJ50	911448	7089	blastx.14	myosin I [Rattus norvegicus]	gi 3724141 emb CAA 50871.1	48% 53% 55% 46% 39% 50%	1009 334 732 863 40 686	1428 681 851 1012 108 715	
HTWFQ19	586124	7091	HMMER 2.1.1	PFAM: Sema domain	PF01403	62.9	14	184	
HTOIA82	844319	7198	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	4.25	50	82	
HTOII14	659280	7204	HMMER	PFAM: Asparaginase	PF01112	20.7	140	217	

HTODM08	960113	7222	blastx.14 2.1.1	(AF106069) deubiquitinating enzyme [Homo sapiens]	gi 5814097 gb AAD5 2099.1 AF106069_1	33%	5	367
HTHBY73	946168	7282	blastx.2	(AK001868) unnamed protein product [Homo sapiens]	dbj BAA91951.1	52% 45%	4 162	183 332
HTGEX10	963862	7305	HMMER 2.1.1	PFAM: SET domain blastx.14	PF00856	105.2	580	960
				(AC005065) determined by GENSCAN prediction and 1	gi 4153862 gb AAD0 4721.1	65% 40%	601 337	1017 477
HTGEA37	908606	7311	blastx.14	(AF001293) aiolos [Mus musculus]	gi 2150044 gb AAB5 8795.1	80%	1	216
HTAIF22	910040	7364	HMMER 2.1.1	PFAM: RhoGEF domain blastx.14	PF00621	29.5	320	394
				(AL022271) similar to Guanine nucleotide exchange 1 1 this g	gi 3876654 emb CAA 18349.1	64%	281	397
HTAIF11	965738	7365	blastx.14	(AF061555) ubiquitin- protein ligase E3-alpha [Mus musculus]	gi 3170887 gb AAC4 0165.1	48% 50%	6 297	293 392
HTAEV23	959129	7369	HMMER 2.1.1	PFAM: WW domain blastx.14	PF00397	25.9	478	386
				This gene is novel. [Homo sapiens]	gi 603953 dbj BAA07 893.1	89%	823	359
HTAEP05	932459	7370	blastx.14	Pro-Pol-dUTPase polyprotein [Mus musculus]	gi 2065210 emb CAA 73251.1	76% 48% 47% 44%	225 406 3 500	275 510 59 553

						77%	386	412
HTABK47	720684	7379	HMMER 2.1.1	PFAM: Monoxygenase	PF01360	23.3	371	430
HSYCV01	940661	7408	HMMER 1.8	PFAM: Hydroxymethylglutaryl- coenzyme A reductase	PF00369	7.29	448	492
HSAWR08	959943	7458	blastx.14	(AL110271) hypothetical protein [Homo sapiens]	gi 5817084 emb CAB 53709.1	98%	123	287
HSAUL84	908440	7504	HMMER 2.1.1	PFAM: gag gene protein p24 (core nucleocapsid protein)	PF00607	43.3	105	302
			blastx.14	gag protein [Human endogenous retrovirus K] 71418.1	gi 1780975 emb CAA 71418.1	83% 60%	135 24	299 152
HNHOF94	948720	7551	blastx.2	(AK00496) unnamed protein product [Homo sapiens]	dbj BAA91205.1	67%	176	484
HNHNP81	928378	7554	HMMER 1.8	PFAM: 7 transmembrane receptor (rhodopsin family)	PF00001	58.09	233	511
			blastx.2	(AF091575) olfactory receptor [Rattus norvegicus]	gb AAC64595.1	61% 52%	236 502	505 618
HNHLC01	915363	7581	blastx.14	unknown protein [Homo sapiens]	gi 1196431 gb AAA8 8036.1	46% 40% 36% 61% 46%	5 57 133 219 260	82 131 207 257 304
HNHGTV62	743400	7603	blastx.2	(AK000385) unnamed protein product [Homo sapiens]	dbj BAA91131.1	62% 76%	52 287	285 349

HNHGE31	698046	7624	HMMER 1.8	PFAM: Zinc-binding metallopeptidase domain	PF00099		3.3	83	109
HNHGV49	975415	7644	blastx.2	hypothetical protein (L1H 3' region) - human	pir B34087 B34087		81% 71% 90%	483 227 217	190 6 188
HNHFH24	903741	7657	HMMER 2.1.1	PFAM: Sodium:neurotransmitter symporter family	PF00209		37.2	208	306
			blastx.14	(AF075266) orphan transporter isoform B9 [Mus musculus]	gi 3347930 gb AAC2 7761.1		76% 27%	187 414	327 467
HNHDF07	953883	7702	HMMER 1.8	PFAM: Fibronectin type III domain	PF00041		7.48	242	319
HNHDC29	904546	7704	blastx.14	contactin associated protein [Homo sapiens]	gi 1857708 gb AAB4 8481.1		98%	219	7
HNHCl32	861673	7716	HMMER 1.8	PFAM: 7 transmembrane receptor (rhodopsin family)	PF00001		133.17	195	545
			blastx.2	(AF112461) G protein- coupled receptor 57 [Homo sapiens]	gb AAF27279.1 AF1 12461_1		100% 100% 100%	189 112 56	551 186 112
HNHCl32	956105	9645	HMMER 1.8	PFAM: 7 transmembrane receptor (rhodopsin family)	PF00001		133.17	951	601
			blastx.2	(AF112461) G protein- coupled receptor 57 [Homo sapiens]	gb AAF27279.1 AF1 12461_1		100% 100% 100%	555 478 422	917 552 478
HNHBf47	949027	7731	HMMER 1.8	PFAM: Cadherin	PF00028		44.76	668	522
			blastx.2	(AB028499) Flamingo 1	dbj BAA84070.1		96%	409	666

[Mus musculus]	5	259
92%	666	923
91%	243	398
86%	412	660
42%	370	660
36%	412	660
36%	666	884
43%	669	896
33%	355	699
43%	666	884
39%	648	890
38%	20	247
32%	11	253
30%	361	648
36%	14	235
39%	654	884
37%	14	247
35%	26	247
35%	666	878
32%	412	699
37%	672	854
28%	433	708
40%	270	380
35%	270	380
37%	270	398
44%	270	371
38%	270	371
33%	264	362
32%	683	829
29%	2	262
57%	723	764
35%	270	374

HNHAF61	742116	7745	HMMER 1.8	PFAM: Cadherin	PF00028		39%	412	480
			blastx.2	(AF152473) protocadherin alpha C1 short form protein [Homo sapiens]	gb AAD43734.1 AF1 52473_1		75% 84% 33% 93% 40%	81 173 87 1 10	677 364 686 84 75
HNHAF61	955094	9649	blastx.14	(AF152303) protocadherin alpha C1 [Homo sapiens]	gi 5456892 gb AAD4 3697.1		98% 40% 42% 32% 100% 77% 37% 225	325 715 499 778 724 867 275	1071 987 660 1023 176 229 275
HNGOZ40	969158	7757	blastx.14	(AF155098) NY-REN-8 antigen [Homo sapiens]	gi 5360091 gb AAD4 2864.1 AF155098_1		30% 89% 35% 40% 36% 50%	496 269 895 568 717 499	684 325 1011 663 791 540
HNGNY02	918626	7769	HMMER 1.8	PFAM: FAD/NAD- binding domain in oxidoreductases	PF00175		78% 4.43	599 366	477 440
HNGND01	915294	7778	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130		2.07	464	490
HNGMW65	950173	7781	blastx.2	(AF010144) neuronal thread protein AD7c-NTP	gb AAC08737.1		62% 67%	340 340	143 248

HNGMD48	974358	7788	HMMER 1.8	PFAM: Cystatin domain	PF00031	6.93	269	349
HNGLY08	948825	7791	blastx.14	(AJ010949) calcium channel alpha-2-delta-C subunit [Mus musculus]	gi 4186073 emb CAA09423.1	79%	219	392
HNGLL07	952236	7795	blastx.14	KERATIN TYPE II CYTOSKELETAL 8 (FRAGMENT).	sp Q29386 Q29386	41% 71% 83% 72%	199 43 77 242	77 2 42 210
HNGKM74	942758	7801	HMMER 1.8	PFAM: HMG (high mobility group) box blastx.2 (AL117470) hypothetical protein [Homo sapiens]	PF00505	5.95	437	526
HNGIR10	964715	7837	blastx.14	NK10 [Mus musculus]	emb CAB55945.1  gi 506502 emb CAA56225.1	40%	2	817

HNGFF50	941480	7879	blastx.14	(AJ010949) calcium channel alpha-2-delta-C subunit [Mus musculus]	gi 4186073 emb CAA .09423.1		45% 61% 57% 37% 26% 39% 46% 50% 33% 30%	193 199 196 178 217 115 181 232 309 306
HNGEO79	951489	7897	HMMER	PFAM: IG (immunoglobulin) superfamily	PF00047		78% 86%	285 986
			blastx	(AF143185) high affinity immunoglobulin gamma Fc 1	gb AAD34946.1 AF1 43185_1		54% 41% 77% 36%	130 921
HNGEI11	967314	7902	blastx.14	pol polyprotein [Baboon endogenous virus]	gi 509838 gb AAA87 332.1		287 404 230 140	385 520 283 214
HNGDM11	967512	7933	blastx.14	reverse transcriptase [Homo sapiens]	gi 439877 gb AAB02 291.1		70% 42% 53%	258 39 324
HNGDA08	959964	7952	HMMER	PFAM: Zinc finger, CCHC class	PF00098		36% 50% 47% 20%	317 152 368 210
HNGAZ08	959977	7973	blastx.14	p40 [Homo sapiens]	gi 2072966 gb AAC5 1272.1		45% 40%	292 205 104 82
								261 284
								391 320 93 19

HNFID11	966347	7997	blastx.14	(AF132948) CCG1-14 protein [Homo sapiens]	gi 4680667 gb AAD2 7723.1 AF132948_1	100%	40% 35%	144 316	100 266			
HNFHR56	733297	8003	HMMER 1.8	PFAM: IG (immunoglobulin) superfamily	PF00047	2.96	200	14	115			
HNEDO77	955894	8051	blastx.14	(AB020063) Keap1 [Mus musculus]	gi 3894323 dbj BAA3 4639.1	90% 44% 42% 38% 44% 100% 27% 85%	384 387 420 339 387 79 402 360	64 91 91 91 232 44 316 346				
HNEBJ81	529571	8067	HMMER 2.1.1	PFAM: N- acetyltransferase	PF00797	40.5	40.5	18	125			
HMWEN61	909931	8125	blastx.14	(AF020313) proline-rich protein 48 [Mus musculus]	gi 2624972 gb AAB9 4880.1	84% 100%	89 89	89 89	307 9			
HMWBTS9	893995	8141	HMMER 1.8	PFAM: 4 transmembrane segments integral membrane proteins	PF00335	27.49	51	51	113			
HMSMN71	927097	8184	HMMER 1.8	PFAM: Ubiquitin family	PF00240	32.11	24	24	200			
HMSJL53	921263	8196	blastx.14	(AF176069) ubiquilin [Homo sapiens]	gi 5733824 gb AAD4 9751.1 AF176069_1	78% 63% 53%	3 550 550	518 606 594				
				decorin (PGII) [Mus musculus]	gi 53669 emb CAA37 876.1	36% 46% 35%	281 48 134	403 131 244				